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Atty Dkt. No.: 10030208-1
USSN: 10/640,081

AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A method for screening a combination of treatments to specifically target a disease process that impacts gene expression, said method comprising the steps of:

(a) providing differential expression levels of predetermined genes of diseased tissue samples relative to at least one reference tissue for respective features of microarrays targeting the predetermined genes, wherein each feature targets a specific gene, said features being used to calculate the differential expression levels;

(b) for each of the respective features of respective microarrays for each diseased tissue sample, providing a single phenotypic/genotypic signature representing the differential expression level for each diseased tissue sample for that feature across the respective microarrays, respectively;

(c) treating the diseased tissue samples with a treatment;

(d) measuring a treatment-response value with respect to each of the diseased tissue samples as effected by the treatment;

(e) generating a single phenotypic signature representing the treatment-response values of each of the diseased tissue samples;

(f) repeating steps (c) – (e) with a different treatment at least once so that multiple phenotypic signatures have been generated for multiple treatments;

(g) performing a clustering operation based on the phenotypic/genotypic signatures of the differential expression levels and the phenotypic signatures of the treatment-response values together; and

(h) selecting treatments by identifying the treatment-response phenotypic signatures caused by those treatments, and which are clustered with phenotypic signatures representing differential expression levels representative of the diseased tissue samples.

2. (Original) The method of claim 1, wherein said providing differential expression levels further comprises processing the diseased tissue samples and the at least one reference tissue using microarray technology to obtain the differential expression levels of the diseased tissues relative to the at least one reference tissue.